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A new species of the Giant Salamander genus *Andrias* (Amphibia, Urodela, Cryptobranchidae) from Yuexi, Anhui, China

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https://zoobank.org/3BA6714D-91BF-406A-8468-761B1D3C7DFA

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Abstract

Chinese giant salamanders (genus *Andrias*), encompassing the largest extant amphibian species in the world, are widespread in China. Several molecular studies have shown that there are several undescribed species of *Andrias*. A new species, *Andrias yaoluopingensis* **sp. nov.**, is described, based on mitochondrial genomes and morphological characteristics from Yuexi County, Anqing City, Anhui Province, China. Morphologically, the new species is characterised by the combination of seven external characters: (1) head and trunk flat, head slightly longer than wide; (2) tubercles above the orbit few and irregularly distributed; (3) eye diameter longer than naris diameter; (4) lateral neck fold discontinuous with body fold at fore-limb insertion; (5) interdigital webbing slightly present; (6) finger length formula FIII > FII > FI > FIV; and (7) dorsum tan in life, darker blotches present on trunk. Molecularly, the new species and an undescribed clade (identified in previous studies) of *Andrias* form an independent clade with strong support (1.00/100) in the phylogenetic trees, based on mitochondrial genomes. The number of species in *Andrias* now reaches six, but cryptic species richness in the Chinese giant salamanders deserves further attention.

Key Words

Andrias yaoluopingensis sp. nov., mitochondrial genomes, morphology, taxonomy, undescribed species

Introduction

Giant salamanders of the genus *Andrias* Tschudi, 1837 (Urodela, Cryptobranchidae) are the largest extant amphibian species in the world, comprising five species (Fei et al. 2012; Fei and Ye 2016; Duret et al. 2025). Currently, the following four species of *Andrias* in China have been recorded: *A. davidianus* (Blanchard, 1871); *A. sligoi* (Boulenger, 1924); *A. jiangxiensis* Lu, Wang, Chai, Yi, Peng, Murphy, Zhang & Che, 2022; and *A. cheni* Xu, Gong, Li, Jiang, Huang & Huang, 2023 (AmphibiaChina 2025). One species, *A. japonicus* (Temminck, 1836) is distributed in Japan (Frost 2025). Several studies suggested that the species richness of Chinese giant salamanders

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is underestimated (Murphy et al. 2000; Yan et al. 2018; Liang et al. 2019; Turvey et al. 2019; Marr et al. 2024). Re-evaluation of *Andrias* species and survey of unexplored areas are likely to reveal overlooked diversity.

Chinese giant salamanders have traditionally been interpreted as a single widespread species *Andrias davidianus*. In recent years, the taxonomic and phylogenetic relationships amongst the genus *Andrias* at species level have undergone several revisions. Yan et al. (2018) suggested the Chinese giant salamander once consisted of at least five distinctive clusters and possibly more unrecognised species, based on mtDNA loci and genomic SNPs. Turvey et al. (2019) removed *A. sligoi* from the synonymy of *A. davidianus* based on morphological data and mitogenomes and re-described the holotype (BMNH 1945.11.7.1) of *A. sligoi* in their supplementary Text S1. Liang et al. (2019) suggested seven distinctive clusters based on additional molecular data. Chai et al. (2022) described *A. jiangxiensis* as a new species based on morphological and molecular evidence. Gong et al. (2023) described *A. cheni* as a new species based on morphological data. Marr et al. (2024) suggested at least seven statistically-resolved Chinese species-level lineages based on mitogenomes. However, the molecular data of this genus from Dabie Mountain region have been poorly studied.

In 2017, during a survey of the Dabie Mountain Range, two specimens of *Andrias* were caught in the wild. After examination, they were found to differ from other described congeneric members in both morphological and molecular characteristics. As a result, we herein describe it as a new species of *Andrias*.

Material and methods

Sampling

Two wild-caught specimens were collected in Macao River from the Yaoluoping National Nature Reserve (31.00°N, 116.08°E; elevation 948 m), Yuexi County, Anqing City, Anhui Province, China (Fig. 1). A small piece of skin from the tail margin was cut off and immediately preserved in 95% ethanol. These samples were then used for DNA analysis. After identifying it as a new species, all specimens were humanely euthanised by the injection of 0.7% tricaine methanesulphonate (MS222) solution (Yang et al. 2023) and fresh liver tissue was extracted and immediately preserved in 95% ethanol. The specimens were fixed in 10% formalin for one day and subsequently preserved in 75% ethanol before being deposited in the Anhui Normal University Museum (voucher numbers: HSA25201, HSA25202). Collections of all animals used for this present study comply with the Wildlife Protection Act of China, following the guidelines and regulations approved by Academic Ethics Committee of Anhui Normal University (approval no. AHNU-ET2025004) and with the permission of Anhui Yaoluoping National Nature Reserve Management Committee.

Morphological examination

External measurements were made for the two specimens of the new species with digital calipers to the nearest 0.01 mm. These 25 measurements are as follows: total length (**TTL**), measured from tip of snout to tip of tail; snout-vent length (**SVL**), measured from tip of snout to posterior edge of vent; head length (**HL**), measured from rear of mandible to tip of snout; head width (**HW**), measured at widest point; greatest diameter of eye (**EL**); snout length (**SL**) from tip of snout to the anterior corner of eye; interocular distance (**IOD**), shortest distance between orbital borders; widest diameter of naris (**NL**); internarial distance (**IND**); distance from front of eye to nostril (**END**); suborbital distance (**SOD**), measured as vertical distance from inferior edge of eye to inferior edge of upper lip; length of fore-limb (**FLL**), measured from point of limb insertion to tip of longest finger; length of posterior limb (**PLL**), measured from point of limb insertion to tip of longest toe; tail length (**TAL**), measured from posterior edge of vent to tip of tail; tail height (**TAH**), greatest height of tail including tail fin; distance between axillae on left-hand side of specimen (**AXD**); first finger length (**FI**), measured from base of second finger to tip of first finger; second finger length (**FII**), measured from base of first finger to tip of second finger; third finger length (**FIII**), measured from base of second finger to tip of third finger; fourth finger length (**FIV**), measured from base of third finger to tip of fourth finger; first toe length (**TI**), measured from base of second toe to tip of first toe; second toe length (**TII**), measured from base of first toe to tip of second toe; third toe length (**TIII**), measured from base of second toe to tip of third toe; fourth toe length (**TIV**), measured from base of third toe to tip of fourth toe; and fifth toe length (**TV**), measured from base of fourth toe to tip of fifth toe.

In addition, morphological data of congeners were obtained from literature and museum abbreviations included the following: Muséum national d'Histoire naturelle, Paris, France (**MNHN**); Natural History Museum, London, U.K. (**BMNH**); and Museum of the Kunming Institute of Zoology, Yunnan, China (**KIZ**).

Molecular phylogeny

Total genomic DNA was extracted from ethanol-preserved liver tissues, using the Qiagen DNEasy blood and tissue extraction kit (Qiagen Inc., Valencia, CA, USA). The phylogenetic relationships within *Andrias* were derived from an analysis of the mitochondrial genomes. Two near-complete mitogenomes (14751-bp, 14271-bp; GenBank Accession Numbers: PV693398–693399) were amplified using nineteen primer pairs as in Liang et al. (2019). All amplifications were performed in 50 µl volume with an initial denaturation period of 3 min at 94 °C, which was followed by 35 cycles of 94 °C for 45 s, primer-specific annealing temperatures of 52–55 °C for 1 min, 72 °C for 1 min and a final extension of 72 °C for 10 min. A negative control with no template DNA was included in each PCR run. The PCR products were purified and sequenced with the same primers. DNA

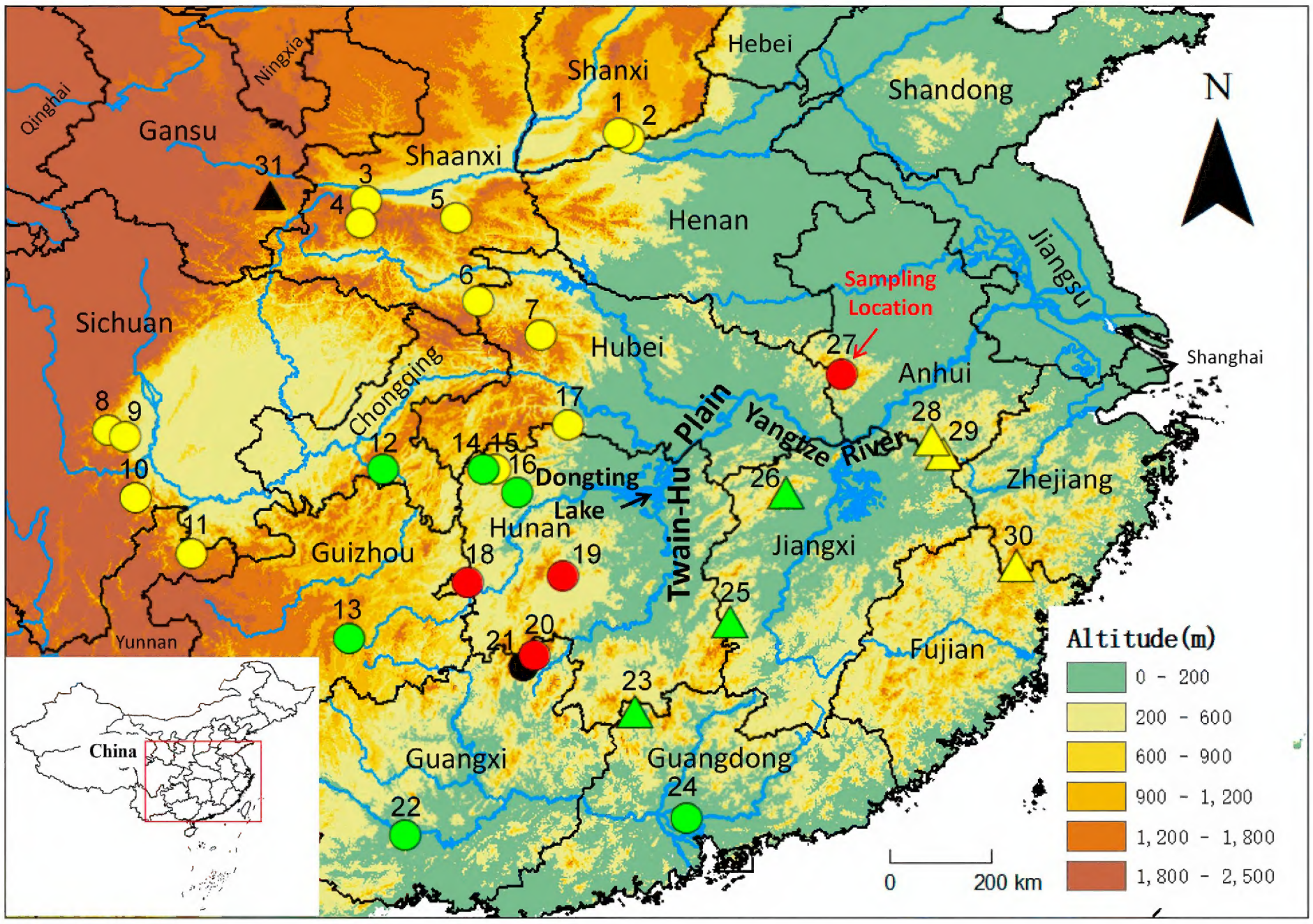

Figure 1. Geographic distribution of the Chinese giant salamanders (species or referred species) of *Andrias* spp. (Liang et al. 2019). Most numbers correspond to those in Table 1. Red circles represent *A. yaoluopingensis* sp. nov.; green circles represent *A. sligoi*; green triangles represent *A. jiangxiensis*; yellow triangles represent *A. cheni*; yellow circles represent *A. davidianus*; black triangle and circle represent two undescribed clades (A and F).

sequencing was performed on an ABI3730 with an ABI-PRISM BigDye Terminator Cycle Sequencing Ready Reaction Kit (PerkinElmer Biosystems, Foster City, CA, USA). For the phylogenetic analyses, 30 mitogenomes from additional Chinese *Andrias* congeners and one mitogenome of the outgroup species *A. japonicus* (Temminck, 1836), were obtained from previous studies and incorporated into our dataset (Liang et al. 2019; Marr et al. 2024). Detailed information is provided in Table 1. Mitogenomes were aligned using MEGA v. 11.0.1 (Kumar et al. 2018) and MAFFT v. 7 with default parameters and manually checked.

The matrilineal genealogy was reconstructed using Bayesian-Inference (BI) and Maximum-Likelihood (ML) methods, based on mitochondrial genomes. PartitionFinder2 was used to test the best partitioning scheme and jModelTest v. 2.1.2 was used to test the best-fitting nucleotide substitution model. The data were analysed using BI in MrBayes v. 3.2.7 (Ronquist et al. 2012) and ML in RaxmlGUI v. 2.0.14 (Silvestro and Michalak 2012). Two independent runs were conducted in a BI analysis, each of which was performed for 10 million generations and sampled every 1000 generations with the first 25% of the samples discarded as burn-in. The analyses used the proportion of invariable sites estimated from the data and 1000 bootstrap pseudoreplicates under the GTR+G substitution model. Nodes in the trees were considered well supported when Bayesian posterior probabilities (BPP) were ≥ 0.95 and ML bootstrap support (BS) was ≥ 70% (Chen et al. 2021).

The sequences of mitochondrial genomes (Table 1) were assigned to their respective species group and generated the haplotypes using DNAsp v.6.0.6 (Rozas et al. 2017; Wang et al. 2023). The network of haplotypes was determined using a statistical analysis of parsimony with TCS (Templeton et al. 1992), implemented in PopART v.1.7 (Leigh and Bryant 2015). Estimates of evolutionary divergence over sequence pairs between and within group mean distances amongst the Chinese salamanders are presented in Table 3, with analyses conducted in MEGA11 (Tamura et al. 2021).

Results

BI and ML analyses resulted in identical topologies (Fig. 2). As shown in the tree, two major clades were identified amongst the Chinese giant salamander samples. The first clade is composed of all described Chinese giant salamanders with strong support (BPP 1.00, BS 100) and an undescribed distinct cluster (clade F). The new species *A. yaoluopingensis* sp. nov. corresponds to clade C (a previously undescribed species) with strong support (BPP 1.00, BS 100). The second major clade is an undescribed cluster (clade A). Based on the mitochondrial genomes of the Chinese giant salamanders,

Table 1. Localities, voucher information (holotype: HSA25201), clade name and GenBank accession numbers for all samples of mitogenomes used in this study.

GenBank no.	Voucher	Clade name	Locality (Numbers)	Species/ Referred Species	Sources
PV693398	HSA25201	C	Yuexi, Anqing, Anhui (27)	*A. yaoluopingensis* sp. nov.	In this study
PV693399	HSA25202	C	Yuexi, Anqing, Anhui (27)	*A. yaoluopingensis* sp. nov.	In this study
KU131042	GSTS240	F	Qinzhou, Tianshui, Gansu (31)	Undescribed	Liang et al. (2019)
KU131043	SCMB244	G	Mabian, Leshan, Sichuan (10)	*A. davidianus*	Liang et al. (2019)
MK177468	NHM1909.7.22.1	G	Ya'an, Sichuan (8)	*A. davidianus*	Turvey et al. (2019)
MK177467	MCZA 2853	G	Hongya, Meishan, Sichuan (9)	*A. davidianus*	Turvey et al. (2019)
MK177466	NMNH 52409	G	Ya'an, Sichuan (8)	*A. davidianus*	Turvey et al. (2019)
KU131057	SXSLZS672	G	Zhashui, Shangluo, Shaanxi (5)	*A. davidianus*	Liang et al. (2019)
KU131061	HNSZSDJ82	G	Sangzhi, Zhangjiajie, Hunan (15)	*A. davidianus*	Liang et al. (2019)
KU131047	SXYQLS371	G	Yuanqu, Yuncheng, Shanxi (1)	*A. davidianus*	Liang et al. (2019)
KU131040	SXTB202	G	Taibaihe, Baoji, Shaanxi (4)	*A. davidianus*	Liang et al. (2019)
KU131058	SXTBYG677	G	Yinge, Taibai, Baoji, Shaanxi (3)	*A. davidianus*	Liang et al. (2019)
KU131048	HNJY385	G	Wangwushan, Jiyuan, Henan (2)	*A. davidianus*	Liang et al. (2019)
KU131053	YNYL551	G	Yiliang, Zhaotong, Yunnan (11)	*A. davidianus*	Liang et al. (2019)
KU131046	GDLZ365	D	Lianzhou, Qingyuan, Guangdong (23)	*A. jiangxiensis*	Liang et al. (2019)
KU131044	JXJA336	D	Jing'an, Yichun, Jiangxi (26)	*A. jiangxiensis*	Liang et al. (2019)
KU131045	JXJGS352	D	Jinggangshan, Ji'an, Jiangxi (25)	*A. jiangxiensis*	Liang et al. (2019)
MK177462	ROM11037	E	Huangshan, Anhui (29)	*A. cheni*	Turvey et al. (2019)
KU131060	AHHS695	E	Xiuning, Huangshan, Anhui (29)	*A. cheni*	Liang et al. (2019)
KX268733	HS16091	E	Qimen, Huangshan, Anhui (28)	*A. cheni*	Xu et al. (2016)
MK177463	ROM 11038	E	Huangshan, Anhui (29)	*A. cheni*	Turvey et al. (2019)
MK177464	ROM 11039	E	Huangshan, Anhui (29)	*A. cheni*	Turvey et al. (2019)
MK177461	ROM 11036	E	Huangshan, Anhui(29)	*A. cheni*	Turvey et al. (2019)
KU131059	ZJLSQY680	E	Qingyuan, Lishui, Zhejiang (30)	*A. cheni*	Liang et al. (2019)
KU131055	GXZY587	C	Ziyuan, Guilin, Guangxi (20)	*A. yaoluopingensis* sp. nov.	Liang et al. (2019)
KU131054	GZGDYX583	B	Guiding, Qiannan, Guizhou (13)	*A. sligoi*	Liang et al. (2019)
MK177469	NHM 1945.11.7.1	B	Hong Kong?	*A. sligoi*	Turvey et al. (2019)
KU131052	HNLS55	B	Longshan, Xiangxi, Hunan (14)	*A. sligoi*	Liang et al. (2019)
KU131051	CQWL481	B	Huolu, Wulong, Chongqing (12)	*A. sligoi*	Liang et al. (2019)
KU131050	HNWMY48	B	Yongding, Zhangjiajie, Hunan (15)	*A. sligoi*	Liang et al. (2019)
MK177465	ZMB 24105	B	Guangdong or Guangxi (22, 24)	*A. sligoi*	Turvey et al. (2019)
KU131056	GXXA609	A	Xing'an, Guilin, Guangxi (21)	Undescribed	Liang et al. (2019)
AB208679	–	–	–	*A. japonicus*	Gene bank

27 haplotypes (h) from 393 sites were obtained and the haplotype diversity (Hd) was 0.98 (Fig. 3). The haplotype network clarified the deep genetic isolation between the new species *A. yaoluopingensis* sp. nov. and the other Chinese giant salamanders. The genetic distances, based on the mitochondrial genomes amongst species of the Chinese giant salamanders, are presented in Table 3.

Morphologically, our collected specimens can be distinguished from all known congeners (holotypes, details in the taxonomic account below), which can be reliably identified by eye diameter longer than naris diameter, tubercles above the orbit few and irregularly distributed, finger length formula FIII > FII > FI > FIV and interdigital webbing slightly present (Figs 4, 5). Morphometric measurements were performed on the specimens from western Anhui and the holotypes of *A. sligoi*, *A. jiangxiensis* and *A. cheni* are listed in Table 2 (Turvey et al. 2019; Chai et al. 2022; Gong et al. 2023). Morphological comparisons are constrained to holotypes only.

Accordingly, combining the results of the morphological examination presented below, phylogenetic analysis and haplotype network, the specimens from western Anhui are regarded as a new species, which is described herein.

Taxonomic account

***Andrias yaoluopingensis* Jiang, Huang, Zhao & Huang, sp. nov.**

https://zoobank.org/92AFCFB9-87B2-4FAB-96AB-90C350890BB8

Figs 4, 5

Notes. Integrative taxonomic approaches were used in this study to describe the new species *Andrias yaoluopingensis* sp. nov. combining mitochondrial genomes and morphological evidences. Meanwhile, potential biogeographic mechanisms (i.e. historical river capture or anthropogenic translocation) were discussed in the Discussion section below.

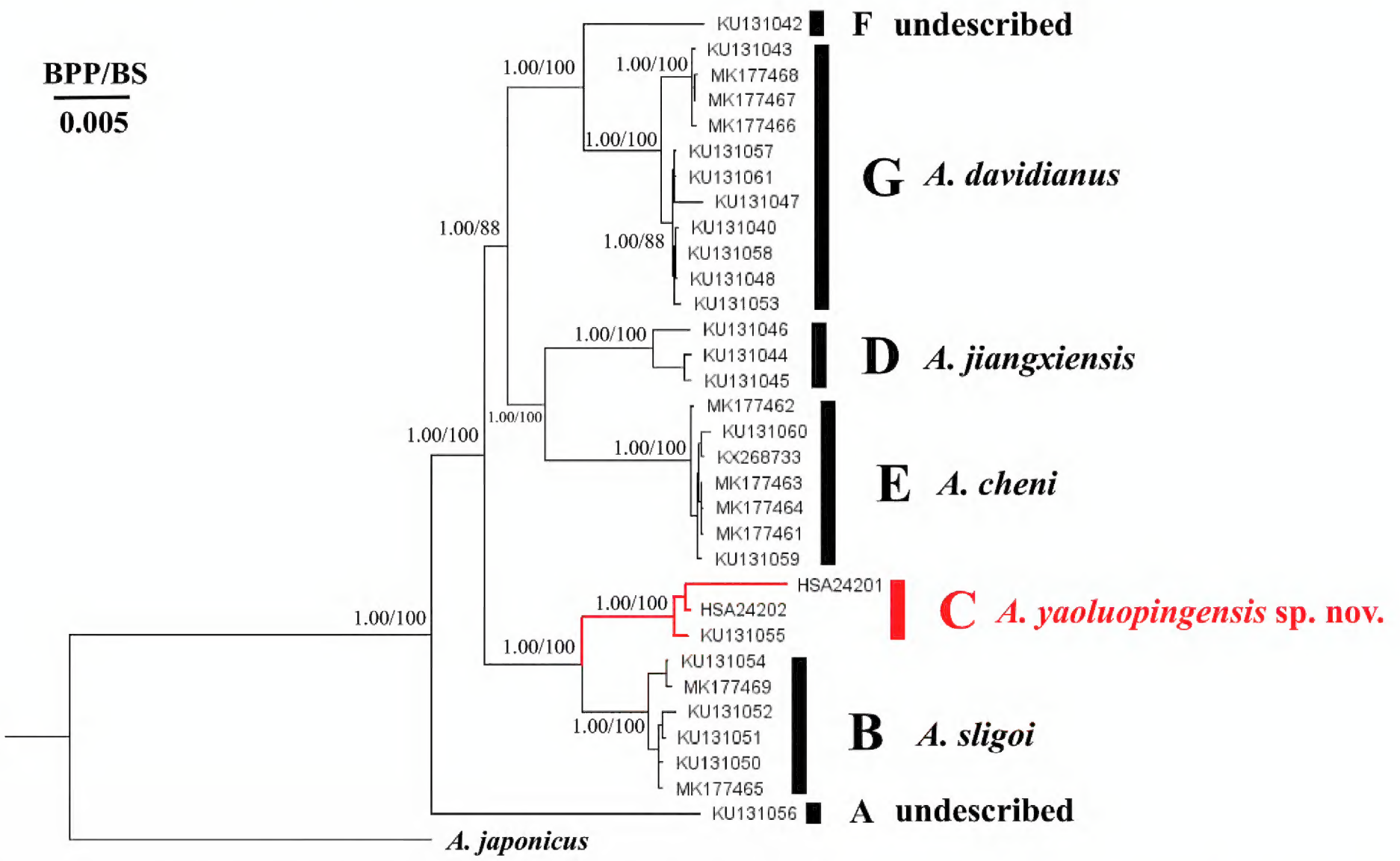

Figure 2. Bayesian-Inference tree and Maximum-Likelihood phylogenies, based on mitochondrial genomes. Bayesian posterior probabilities and the bootstrap supports (BPP/BS) are shown near the nodes. Number at the ends of the lineages correspond to the vouchers in Table 1, HSA24201 and HSA24202 are newly-added vouchers in this study.

Table 2. Morphometric measurements (in mm) of *A. yaoluopingensis* sp. nov. in this study and other Chinese congeners (holotypes, except *A. davidianus*).

	***A. yaoluopingensis* sp. nov.**		***A. sligoi***	***A. jiangxiensis***	***A. cheni***
	HSA25201♂	**HSA25202♀**	**BMNH1945.11.7.1**	**KIZ 037731♂**	**HSA18037♂**
	Holotype	**Paratype**	**Holotype**	**Holotype**	**Holotype**
TTL	650.69	545.80	936.00	589.00	791.00
SVL	420.54	354.13	596.00	381.00	515.00
HL	119.66	112.95	184.00	92.90	128.50
HW	117.70	109.72	152.00	90.90	123.30
EL	4.38	4.65	5.00	4.20	5.00
SL	37.31	30.32	–	–	33.40
IOD	60.21	51.05	81.00	46.80	61.40
NL	2.20	1.44	5.00	1.50	2.40
IND	18.36	13.85	33.00	14.80	22.40
END	36.95	28.71	51.00	27.60	38.60
SOD	20.32	15.16	–	9.50	11.40
FLL	78.59	60.69	105.00	56.10	86.73
PLL	88.20	76.30	168.00	71.50	100.20
TAL	280.90	175.36	340.00	208.00	276.00
TAH	73.64	53.36	89.00	76.20	64.00
AXD	219.30	172.83	297.00	199.00	228.00
FI	13.52	8.21	14.00	7.20	9.12
FII	14.40	11.97	16.00	10.10	14.41
FIII	16.52	12.86	14.00	8.50	28.83
FIV	11.66	8.23	12.00	6.50	10.26
TI	8.45	7.08	19.00	5.90	8.21
TII	14.62	12.58	26.00	11.10	14.39
TIII	18.35	16.21	33.00	13.50	18.66
TIV	17.54	14.86	31.00	12.20	17.43
TV	12.70	10.62	23.00	6.70	8.89

Table 3. Estimates of evolutionary divergence over sequence pairs between and within group mean distances amongst the Chinese salamanders (in 0.01%). The number of base differences per site from averaging over all sequence pairs between and within groups are shown. All ambiguous positions were removed for each sequence pair (pairwise deletion option).

ID	Species	1	2	3	4	5	6	7
1	*A. yaoluopingensis* sp. nov.	0.54						
2	*A. sligoi*	1.31	0.16					
3	*A. jiangxiensis*	2.50	2.17	0.34				
4	*A. cheni*	2.18	1.76	1.55	0.05			
5	*A. davidianus*	2.37	1.97	1.95	1.77	0.18		
6	Clade A	3.11	2.78	2.95	2.76	2.81	-	
7	Clade F	2.57	2.20	2.16	1.97	1.29	3.00	-

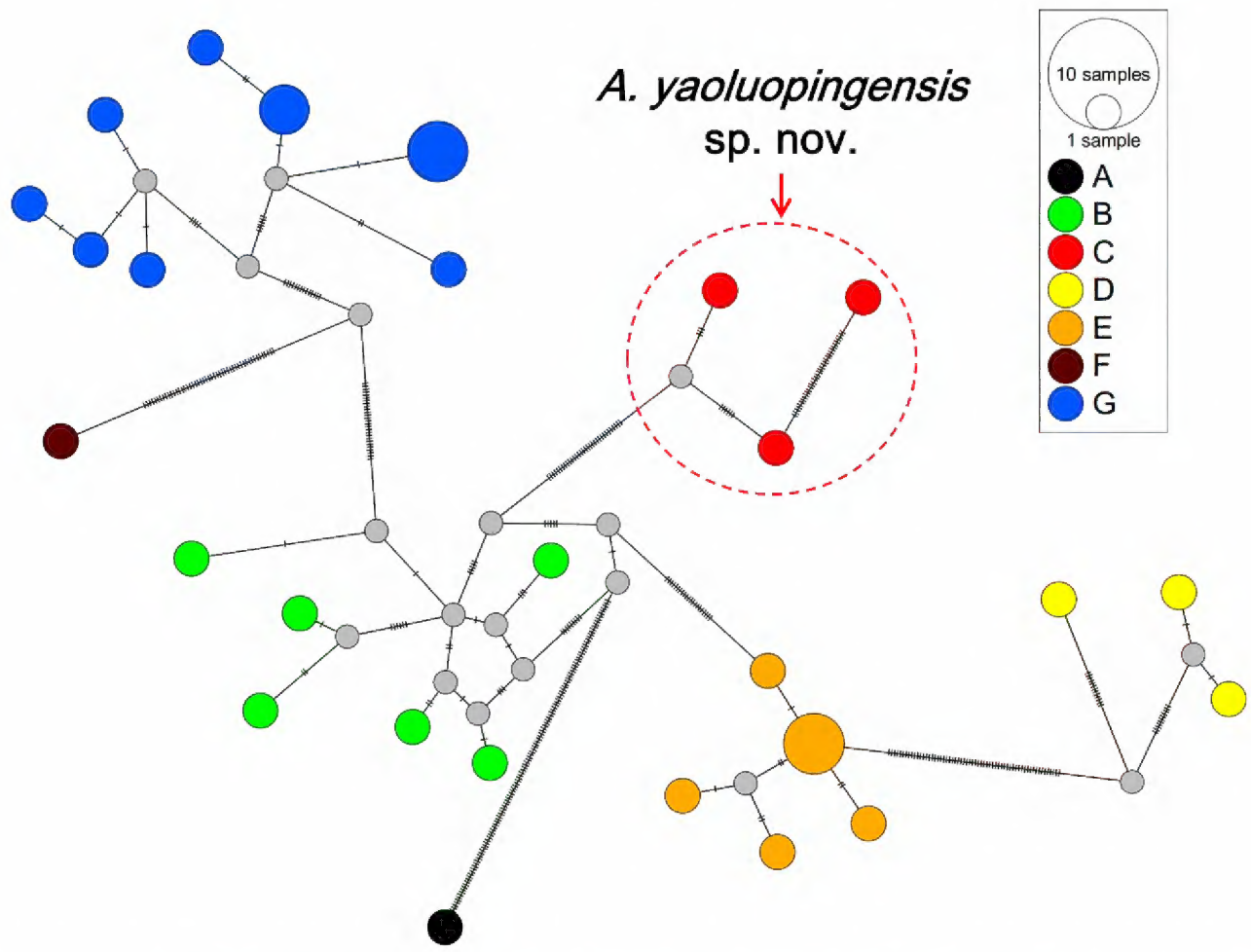

Figure 3. Haplotype network of the Chinese giant salamanders. Different coloured circles represent different species. Red circles and C represent *A. yaoluopingensis* sp. nov.; green circles and B represent *A. sligoi*; yellow circles and D represent *A. jiangxiensis*; orange circles and E represent *A. cheni*; blue circles and G represent *A. davidianus*; black circle and brown circle represent two undescribed clades (A and F); grey circles represent predicted haplotypes.

Type material. ***Holotype.*** • HSA25201, adult male from Macao River, Yaoluoping National Nature Reserve (31.00°N, 116.08°E; elevation 948 m), Yuexi County, Anqing City, Anhui Province, China, collected by Kai ZHAO on 20 September 2017. ***Paratype.*** • An adult female HSA25202. Same collection date and locality as the holotype.

Etymology. The specific name *yaoluopingensis* refers to the type locality of the new species in Yaoluoping National Nature Reserve, Anhui, China. For the English common name, we suggest "Yaoluoping Giant Salamander" and for the Chinese name, 鹞落坪大鲵 (yào luò píng dà ní).

Diagnosis. An *Andrias* species having: (1) head and trunk flat, head slightly longer than wide; (2) tubercles above the orbit few and irregularly distributed; (3) eye diameter longer than naris diameter; (4) lateral neck fold discontinuous with body fold at fore-limb insertion; (5) interdigital webbing slightly present; (6) finger length formula FIII > FII > FI > FIV; and (7) dorsum tan in life, darker blotches present on trunk.

Description of the holotype. HSA25201 (Figs 4, 5), adult male, body flat (TTL 650.69 mm, SVL 420.54 mm). Head large, flat; snout truncate dorsally, obtusely protruding in lateral view; naris rounded and conspicuous; eyes rounded, dorsolaterally positioned, lacking lids; eye diameter longer than naris diameter; internarial distance subequal to interorbital distance; interorbital space between tip of snout flat; large rounded temporal protuberance behind each eye; labial fold indistinct; gular fold present; costal folds on both sides of specimen; dorsolateral folds distinct; lateral neck fold discontinuous with body fold at fore-limb insertion; tubercles above the orbit few and irregularly distributed; ventral surface of trunk smoother than dorsum; four short fin-

Figure 4. Holotype of *Andrias yaoluopingensis* sp. nov. (HSA25201) in life. **A.** Dorsal view; **B.** Lateral view (right side); **C.** Ventral view (Photographed by Zhihao Jiang and Song Huang).

gers, interdigital webbing slightly present, finger length formula FIII > FII > FI > FIV; posterior edge of FIV with dermal fold which is continuous with dermal fold on arm; toe length formula TI < TV < TII < TIV < TIII; callous present on plantar surface below FI and TI; vent slit-like; tail muscular, thick at base, gradually flattening posteriorly and distally.

Colouration of the holotype. Dorsum tan in life, darker blotches present on trunk, gradually decreasing and broken from mid-body to head, limbs and tail, a few black spots scattered between large patches; ground colour of the ventral surface greyish-brown, darker blotches present, anterior venter of head black. In preservative, dorsum and ventral surface faded, with black patches and spots remaining distinct; horny epidermis on tips of fingers and toes as well as palms and soles greyish-white.

Variation. No significant differences in morphology and colouration were found amongst all adult specimens in this study. The paratype (female, TAL/ SVL 0.50) is smaller than the holotype (male, TAL/ SVL 0.67). However, the number of specimens in this study is limited.

Comparisons. Pure *A. davidianus* and *A. sligoi* have not been genetically identified and farm-bred individuals exhibit genetic contamination because of translocated animals or hybrids of *Andrias* spp. (Yan et al. 2018; Chai et al. 2022). As a result, morphological comparisons in recent studies are often based on holotypes (Chai et al. 2022; Gong et al. 2023).

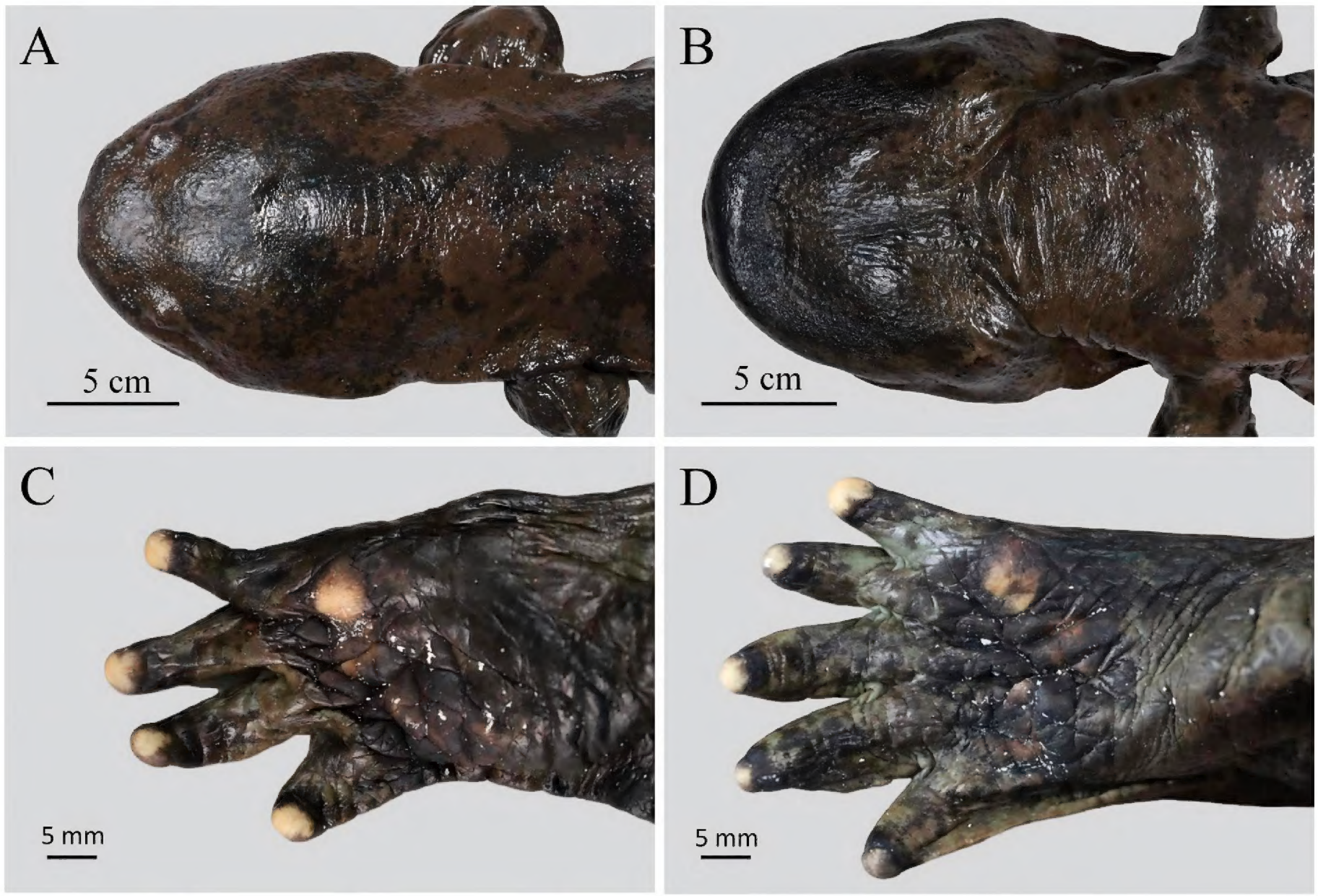

Figure 5. Holotype of *Andrias yaoluopingensis* sp. nov. (HSA25201). **A.** Dorsal view of head; **B.** Ventral view of head; **C.** Ventral view of left fingers; **D.** Ventral view of left toes (Photographed by Zhihao Jiang and Song Huang).

Andrias yaoluopingensis sp. nov. is phylogenetically close to *A. sligoi*, which is distributed in southern China. However, the new species differs from *A. sligoi* by its eye diameter longer than naris diameter (vs. eye diameter equal to naris diameter), finger lengths formula FIII > FII > FI > FIV (vs. FII > FI = FIII > FIV) and interdigital webbing slightly present (vs. interdigital webbing absent) (Turvey et al. 2019).

In addition, *A. yaoluopingensis* sp. nov. further differs from the remaining congeners (Chai et al. 2022; Gong et al. 2023), as follows:

A. yaoluopingensis sp. nov. differs from *A. davidianus* (holotype MNHN-RA-0.7613, images posted on: http://coldb.mnhn.fr/catalognumber/mnhn/ra/0.7613) by its tubercles above the orbit being few and irregularly distributed (vs. head and lower jaw rough, with distinct, regularly arranged tubercles) and FIII longer than FII (vs. FIII shorter than FII).

A. yaoluopingensis sp. nov. differs from *A. jiangxiensis* by its tubercles above the orbit being few and irregularly distributed (vs. smooth skin on the snout and around eyes) and FIII longer than FII (vs. FIII shorter than FII).

A. yaoluopingensis sp. nov. differs from *A. cheni* by its interdigital webbing slightly present (vs. interdigital webbing absent) and FIII longer than FII (vs. FIII shorter than FII).

A. yaoluopingensis sp. nov. differs from *A. japonicus* by its smoother head with indistinct tubercles (vs. dense, distinct, large tubercles).

Distribution and habitat. Based on the phylogenetic analysis, *A. yaoluopingensis* sp. nov. is currently known from the type locality in the Yaoluoping National Nature Reserve in western Anhui, northern Guangxi and Hunan Province. The specimens were caught in a river at 948 m a.s.l., with many crevices between the stones (Fig. 6).

Discussion

The Twain-Hu Plain is located in eastern and southern Hubei, as well as eastern and northern Hunan. Dongting Lake is located in the middle of the Twain-Hu Plain and the Yangtze River runs through it. Clade B (*A. sligoi*) and clade C (*A. yaoluopingensis* sp. nov.) were estimated to have diverged around the Pliocene or early Pleistocene (Liang et al. 2019). During that time, frequent river capture and change were present in the Twain-Hu Plain (Jia et al. 2010; Li et al. 2025). The previously undescribed clade C is adjacent to the southwest corner of the Twain-Hu Plain and the sampling site in this study is adjacent to the northeast corner of the Twain-Hu Plain, which suggests that *A. yaoluopingensis* sp. nov. is located in and around the Twain-Hu Plain. The Chinese giant salamanders (wild-caught populations) in north-eastern Hunan and eastern Hubei need further study.

The lack of nuclear data in our analysis is a shortcoming of our study, as in *Andrias* mitochondrial introgression may happen and thus result in a different taxonomic scenario (Marr et al. 2024), even if recent analysis with nuclear recombinase activating gene 2 (RAG2) revealed

Figure 6. Holotype of *Andrias yaoluopingensis* sp. nov. (HSA25201). **A.** Dorsalateral view in life; **B.** Environment of the sampling location (Photographed by Zhihao Jiang and Kai Zhao).

no obvious geographic patterns (Liang et al. 2019). The major limitation to include such data in our study is the fact that nuclear data from important specimens such as *A. sligoi* holotype and most of the populations are currently unavailable (Turvey et al. 2019). Further sampling is needed to gather this nuclear data and review the whole phylogenetic and biogeographic history of the Chinese *Andrias*. However, given the congruence of the results from the analysis of the available data, we feel confident in proceeding with the formal description of this new species.

The Chinese giant salamanders used to be widely distributed in China, occurring across multiple river basins and montane ecoregions (Fei et al. 2006; Xu et al. 2018; Hara et al. 2023; Nishikawa et al. 2024). The population numbers of Chinese giant salamanders have declined across China primarily due to overexploitation as well as habitat loss and degradation (Wang et al. 2004). For this critically endangered organism, more field surveys and further classification at the species level are necessary and urgent.

With the addition of the new species *A. yaoluopingensis* sp. nov. described here, the genus *Andrias* now includes six species. This study provides relatively complete morphological and molecular data, which can serve as a reference for the conservation of giant salamanders from different lineages, genetic management and enhancement and release of artificial populations.

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